

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 12:21:43 ; Search time 2513 Seconds

(without alignments)

16625.306 Million cell updates/sec

Title: US-10-082-894-1

Perfect score: 1719

Sequence: 1 gtttaattaccgaatttga.....aatctccgtataaaaatt 1719

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: em\_estb1:\*
- 2: em\_estb2:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vri:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	532.2	31.0	537	9	AW783013		AW783013 ra22d01.y
2	511.8	29.8	556	10	BE239174		BE239174 MD0830 Me
3	320.8	18.7	650	9	AW152739		AW152739 JALSL3C10
4	301.4	17.5	327	9	AW589077		AW589077 ra08c01.y

5	300.8	17.5	677	12	BJ112231	BJ112231
6	292.6	17.0	655	9	AU204921	AU204921
7	290.6	16.9	652	12	BJ121936	BJ121936
8	287.6	16.7	649	12	BJ108160	BJ108160
9	283	16.5	647	14	CB374256	CB374256
10	278.2	16.2	285	13	BQ613449	BQ613449
11	277.2	16.1	580	12	BJ116367	BJ116367
12	272.8	15.9	623	12	BJ107746	BJ107746
13	271.4	15.8	620	12	BJ107756	BJ107756
14	270.6	15.7	726	12	BJ155870	BJ155870
15	269.8	15.7	621	12	BJ117851	BJ117851
16	269.2	15.7	623	12	BJ125855	BJ125855
17	269.2	15.7	651	12	BJ126726	BJ126726
18	261.8	15.2	584	12	BJ124149	BJ124149
19	261.8	15.2	585	12	BJ113563	BJ113563
20	261.8	15.2	596	12	BJ101770	BJ101770
21	260.2	15.1	544	12	BJ120572	BJ120572
22	259.8	15.1	621	10	BF423140	BF423140
23	258.2	15.0	557	9	AU207271	AU207271
24	257.4	15.0	592	9	AU205988	AU205988
25	255.6	14.9	686	14	CB013135	CB013135
26	246.2	14.3	791	12	BJ154227	BJ154227
27	241	14.0	700	9	AA629457	AA629457
28	240.4	14.0	552	12	BJ109590	BJ109590
29	238.2	13.9	521	14	M88904	M88904
30	237.2	13.8	759	12	BJ148082	BJ148082
31	230.2	13.4	471	12	BI773091	BI773091
32	229.8	13.4	748	12	BJ141355	BJ141355
33	225.2	13.1	561	12	BJ103886	BJ103886
34	224.6	13.1	476	9	AA273165	AA273165
35	224.4	13.1	745	12	BJ150141	BJ150141
36	224.2	13.0	506	9	AI065990	AI065990
37	224.2	13.0	561	9	AU208103	AU208103
38	223.6	13.0	764	9	AW332502	AW332502
39	222.8	13.0	736	12	BJ149541	BJ149541
40	222.8	13.0	739	12	BJ148716	BJ148716
41	220.4	12.8	602	12	BI174231	BI174231
42	220.2	12.8	546	14	CB403894	CB403894
43	220	12.8	557	10	BE899657	BE899657
44	219.6	12.8	607	9	AU222303	AU222303
45	219.2	12.8	542	9	AU209097	AU209097

ALIGNMENTS

RESULT 1	AW783013	537 bp	linear	EST 10-MAY-2001
LOCUS	ra22d01.y1	Bird-Rao	Meloidogyne incognita J2	Meloidogyne incognita
DEFINITION	CDNA 5' similar to WP:F57B10.3	CELL302	PHOSPHOGLYCERATE MUTASE ;	
ACCESSION	AW783013			
VERSION	AW783013.1	GI:7797619		
KEYWORDS	EST			
SOURCE	Meloidogyne incognita (southern root-knot nematode)			
ORGANISM	Meloidogyne incognita			
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.			
AUTHORS	McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarisvill, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.			
TITLE	The Washington Univ. Nematode EST Project, 1999			
JOURNAL	Unpublished			
COMMENT	Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Uma Rao and David Bird  
(david\_bird@wustl.edu) at North Carolina State University. DNA  
Sequencing by: Washington University Genome Sequencing Center St.  
Louis.  
Seq primer: T3 ET from Amerham  
High quality sequence stop: 419.  
Location/Qualifiers  
1. .537  
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/db\_xref="taxon:6306"  
/dev\_stage="enriched for 2nd stage juveniles"  
/lab\_host="XLOL"  
/clone\_lib="Bird-Rao Meloiodogone incognita J2"  
/note="Vector: ZAP express - pBRCMV (Stratagene); Site 1:  
EcoRI; Site 2: XhoI; Oligo (dT) primed library. cDNA was  
constructed and cloned unidirectionally into the vector  
within the 5' EcoRI and 3' XhoI sites. This library was  
constructed by Dr. Uma Rao and Dr. David Bird at North  
Carolina State University."  
BASE COUNT 152 a 92 c 123 g 170 t  
ORIGIN  
Query Match 31.0%; Score 532.2; DB 9; Length 537;  
Best Local Similarity 99.4%; Pred. No. 1.2e-118;  
Matches 534; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 580 ACTGGACGTTATTATGATGGATGGACAAAGATGGGCGTATTAGATGGCTTAT 639  
Db 1 ACTGGACGTTATTATGATGGATGGACAAAGATGGGCGTATTAGATGGCTTAT 60  
QY 640 GAGGCAATTTGGGAGGTATTGACAAAAGCCACCGTTGTAAGCTCTCATGTTGT 699  
Db 61 GAGGCAATTTGGGAGGTATTGACAAAAGCCACCGTTGTAAGCTCTCATGTTGT 120  
QY 700 AGAGCGGATATGCTCAATCTGAGACTGACGATTTCTGAACCAATCTGTTTTCGGAC 759  
Db 121 AGAGCGGATATGCTCAATCTGAGACTGACGATTTCTGAACCAATCTGTTTTCGGAC 180  
QY 760 GATGGCGAGTAAAGATGACGATCTTTATTTTCTCAATATGCTGCTGATCGTATG 819  
Db 181 GATGGCGAGTAAAGATGACGATCTTTATTTTCTCAATATGCTGCTGATCGTATG 240  
QY 820 CGTCAATTTGTAATTTGGTCTCGAACGTTATTAAGATCTTAATAGTTTCGGTTCCT 879  
Db 241 CGTCAATTTGTAATTTGGTCTCGAACGTTATTAAGATCTTAATAGTTTCGGTTCCT 300  
QY 880 CACCCTAAATATTCAGATTAGTGGATGACCCCAATACAAAGAGTTTCCATTTC 939  
Db 301 CACCCTAAATATTCAGATTAGTGGATGACCCCAATACAAAGAGTTTCCATTTC 360  
QY 940 TCGTTATTCACCTGTGACTCATATGCTTGTGCTGAATGGCTTCTCTCAAGGA 999  
Db 361 TCGTTATTCACCTGTGACTCATATGCTTGTGCTGAATGGCTTCTCTCAAGGA 420  
QY 1000 GTTACTCAATTTCACTGCGGAAACTGAGAAGTATCCTCATGTTACCTTCTTTTAT 1059  
Db 421 GTTACTCAATTTCACTGCGGAAACTGAGAAGTATCCTCATGTTACCTTCTTTTAT 480  
QY 1060 GGTGTCGAGAAGTTCAATTTCAAGATGAAGAGCGTTGTATGTTCCGTCACCAAAA 1116  
Db 481 GGTGTCGAGAAGTTCAATTTCAAGATGAAGAGCGTTGTATGTTCCGTCACCAAGA 537  
RESULT 2  
BE239174 556 bp mRNA linear EST 11-JUL-2000  
LOCUS  
DEFINITION  
MD0830 Meloiodogone incognita J2 (#MD99-1) Meloiodogone incognita  
cDNA clone 3739 5' similar to phosphoglycerate mutase (AF039713),  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BE239174 GI:9034138  
EST.  
Meloiodogone incognita (southern root-knot nematode);  
Meloiodogone incognita  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heteroderidae; Meloiodogyninae; Meloiodogone.  
1 (bases 1 to 556)  
Dautova, M., Gommers, F.J., Bakker, J. and Smant, G.  
5' end expressed sequence tags from Meloiodogone incognita  
preparasitic J2 cDNA library  
Unpublished (2000)  
Contact: Smant G / Dautova M  
Laboratory of Nematology  
Wageningen University and Research Center  
Box 8123, Binnenhaven 10, 6709 PD Wageningen, The Netherlands  
Tel: 31 317 485 254  
Fax: 31 317 484 254  
Email: Geert.Smant@medew.nema.wau.nl,  
Makedonka.Dautova@medew.nema.wau.nl  
Insert Length: 556 Std Error: 0.00  
Seq primer: T7 promoter primer  
High quality sequence stop: 556.  
Location/Qualifiers  
1. .556  
/organism="Meloiodogone incognita"  
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/db\_xref="taxon:6306"  
/clone="3739"  
/dev\_stage="second stage parasitic juveniles (J2)"  
/clone\_lib="Meloiodogone incognita J2 (#MD99-1)"  
/note="Vector: pMAK1; Site 1: Sfi IA; Site 2: Sfi IB; cDNA  
was synthesized using SMART III oligo, CDS III oligo d(T  
30 (Clontech) and Superscript II reverse transcriptase  
(Life Technology). cDNA clones were size fractionated and  
directionally ligated in the Sfi IA restriction site at  
5' end and Sfi IB at 3' end of pMAK1. pMAK1 was derived  
from the plasmid pcDNA II (Invitrogen)."  
BASE COUNT 161 a 113 c 124 g 158 t  
ORIGIN

Query Match 29.8%; Score 511.8; DB 10; Length 556;  
Best Local Similarity 99.1%; Pred. No. 1.1e-113;  
Matches 546; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

QY 994 CAAGAGTTACTCAATTTTCACTGTCGGAAACTGAGAACTATCCTCATGTTCTTCTTC 1053  
Db 9 CAAGAGTTACTCAATTTTCACTGTCGGAAACTGAGAACTATCCTCATGTTCTTCTTC 68  
QY 1054 TTAAATGGTGGTCGAGAAGTTCAATTCGAAGATGAAGAGCGTTGTATGTTCCGTCACCA 1113  
Db 69 TTAAATGGTGGTCGAGAAGTTCAATTCGAAGATGAAGAGCG-TGTATGTTCCGTCACCA 127  
QY 1114 AAAGAAGTTGCTACATATGATTTAAACCCAGAAATGAATGCTGAGTTTCCGCAAAA 1173  
Db 128 AAAGAAGTTGCTACATATGATTTAAACCCAGAAATGAATGCTGAGTTTCCGCAAAA 187  
QY 1174 ATGGTCGACCAATTTGAGTCAGGAGGATCCTTTGGTTATGTGCAATTTTGGCGCTCT 1233  
Db 188 ATGGTCGACCAATTTGAGTCAGGAGGATCCTTTGGTTATGTGCAATTTTGGCGCTCT 247  
QY 1234 GACATGGTTGGACATCTGTTAAATTTGAACCTGCGCTCAAGCATGTCAAGCTACTGAC 1293  
Db 248 GACATGGTTGGACATCTGTTAAATTTGAACCTGCGCTCAAGCATGTCAAGCTACTGAC 307  
QY 1294 GAGCAATTTGGAAGATATTTGAAGCATGCCAAACTTATAATACGTTCTTATGGTTACT 1353  
Db 308 GAGCAATTTGGAAGATATTTGAAGCATGCCAAACTTATAATACGTTCTTATGGTTACT 367  
QY 1354 TCCGATCATGGAATGCTGAGAGATGATGTCCTCCGATGGTAGTGAACATACTGCACAT 1413  
Db 368 TCCGATCATGGAATGCTGAGAGATGATGTCCTCCGATGGTAGTGAACATACTGCACAT 427

QY 1414 ACCGCAATTTGGCCCACTTTACTTGTCTTCCAAAACATTTGTTTTAAATCGACTCCA 1473  
|||||  
Db 428 ACCTGCAA-TTGGTCCCACTTTACTTGTCTTCCAAAACA-TTGTITTTAAATCGACTCCA 485  
QY 1474 CCTACTGAGATGATGGCAAGACAGTGCACGAGCCTTACGTGATGTTGACCGACTGTT 1533  
|||||  
Db 486 CCTACTGAGATGATGGCAAGACAGTGCACGAGCCTTACGTGATGTTGACCGACTGTT 545  
QY 1534 CTACAATTAAT 1544  
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Db 546 CTACAATTAAT 556

RESULT 3  
AW152739  
LOCUS  
DEFINITION  
JALSL3C109SAC Litomosoides sigmodontis (parasitic nematode)  
infective L3 Litomosoides sigmodontis cDNA clone JALSL3C109 5',  
mRNA sequence.  
ACCESSION  
AW152739.1 GI:6200684  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Litomosoides sigmodontis  
Litomosoides sigmodontis  
Onchocercidae; Litomosoides.  
REFERENCE  
1 (bases 1 to 650)  
AUTHORS  
Allen, J.E., Daub, J., Guillian, D., McDonnell, A., Lizotte-Waniewski,  
, M., Taylor, D.W. and Blaxter, W.  
TITLE  
Analysis of genes expressed at the infective larval stage validates  
utility of Litomosoides sigmodontis as a murine model for filarial  
vaccine development  
JOURNAL  
Infect. Immun. 68 (9), 5454-5458 (2000)  
MEDLINE  
20407372  
PUBMED  
10948183  
COMMENT  
Contact: Allen JE  
Institute of Cell, Animal and Population Biology  
University of Edinburgh  
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9  
3JT, UK  
Tel: +44 131 650 7014  
Fax: +44 131 670 5450  
Email: j.allen@ed.ac.uk  
The Litomosoides EST dataset (including the LSC clustering  
information) is available on the www at [http://www.ed.ac.uk/\(tilde\)mbx/LitoWeb/LitoESTs.html](http://www.ed.ac.uk/(tilde)mbx/LitoWeb/LitoESTs.html)  
PCR Primers  
FORWARD: 17PL (CTCACTATAGGCGGAATTGG)  
BACKWARD: M13 Forward (CGCCAGGTTTCCCGATCAGCAGC)  
Seq primer: SAC (GGGAACAAGCTGGAG).  
Location/Qualifiers  
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infective L3"  
/note="Vector: Lambda Zap II; Site\_1: EcoRI (5'end);  
Site\_2: XhoI (3'end); Litomosoides sigmodontis is a  
filarial nematode parasite of rats. The library was  
constructed from vector-(Ornithonyssus bacoti) derived L3  
for Prof. David Taylor at the Centre for Tropical  
Veterinary Medicine, Edinburgh, UK"

BASE COUNT 202 a 126 c 152 g 170 t  
ORIGIN  
Query Match 18.7%; Score 320.8; DB 9; Length 650;  
Best Local Similarity 69.3%; Fred. No. 4.1e-67;  
Matches 452; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY 788 TTATTTCTCAATTTATCGTGTATCGTATCGTCAAAATTTGTAATTTGGTGTCTCG 847  
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Db 2 TGATATCTTTCGATTTATCGCTGACCGCATCGGGGAATCACTGAATGTATGGTATG 61  
QY 848 AACGTTTAAAGATCTTAATAGTTCGGTTCCTCACCTTAAATAATTTAGATTTAGTGGGA 907  
|||||  
Db 62 AACGATACAAAGATCTGAAGTCTGATATTAACACCCGGAAGATATGCAAGTAGTTGGGA 121  
QY 908 TGACCCATACAATAAGAGTTTCCATTTCCATTCCTTATCCACCTGTGACTCATCTA 967  
|||||  
Db 122 TGACTCAGTACAAGCAGAAATTTACATTTCTGCTGCTCTTTCCACCAAGATTCATAAAA 181  
QY 968 ATGTGCTTGTCTGAATGGCTTGTCTCTCAAGGAGTTTACTCAATTTTCACTGTGCGAAACTG 1027  
|||||  
Db 182 ACGTATTTGGCCGAATGGTTATCTGTAACAATTTAACACAGTTCCATTTGTCAGAAACGG 241  
QY 1028 AGAAGTATCTTCATGTTTACCTTCTTTTAAATGTTGGTGCAGAAATTTCAATTTCCAAGATG 1087  
|||||  
Db 242 AAAAATATCGGCACGCTCATATTTCTTTTCAACGGCGGTGTGGAGAAACAATTTGGGAATG 301  
QY 1088 AAGAGCGTTGATGTTCCGTCCACCAAGAGTTTCTACATATGATTTAAACACGAAA 1147  
|||||  
Db 302 AAGAACGGTGTGTTAGTGTGACCGA---AAGTTGTACCTATGATCTTGATCCACCAA 358  
QY 1148 TGAATGCTCTGGAGTTGCCGAAAAAATGGTCGAGCAAAATTTGAGTCAGCAGCATCTCT 1207  
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Db 359 TGAGCTCAGCAGGTCTGGCTGATAGTTTATCGACCAATTCATCTAAGAAACATCCAT 418  
QY 1208 TGGTTATGCAATTTTGGCTCTCTGACATGTTGGACATCTGGTAAATTTGAACCTG 1267  
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Db 419 TTGTCATGTCAATTTTGGCTCTCTGATGTTGGCCATCTACTGCGCTATATGAAGCGG 478  
QY 1268 CGCTCAAGCATGTCAAGCTACTGACGAGGCAATTTGGAAGATTTTGAAGCATCCAAA 1327  
|||||  
Db 479 CGGTGAAAGCAGTTGAGGCAACAGATATGCTATTGGAGATATATGAGCATGTAAGA 538  
QY 1328 CTTATATTTACGTTCTTATGTTTACTTCCGATCATGGAATGCTGAGAGATGATTTGCTC 1387  
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Db 539 AGAAGCAGTACATATTTGATGTTGTAACAGCAGATCATGGCAATGCTGAAAAAATGATGGCG 598  
QY 1388 CCGATGGTAGTGAACATCTACTGCACATCTGCAATTTGGTCCATTTACTTG 1439  
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Db 599 CAGATGGTAGCAAGCATACTGCCACACATGCAATTTGGGCGCATTCACCTG 650

RESULT 4  
AW589077  
LOCUS  
DEFINITION  
ra08c01.y2 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita  
cDNA 5' similar to WP:F57B10.3 CE11302 PHOSPHOGLYCERATE MUTASE ;,  
mRNA sequence.  
ACCESSION  
AW589077  
VERSION  
AW589077.1 GI:7276048  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
Meloidogyne incognita (southern root-knot nematode)  
Meloidogyne incognita  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heteroderidae; Meloidogyinae; Meloidogyne.  
REFERENCE  
1 (bases 1 to 327)  
AUTHORS  
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,  
Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,  
Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarelshvili, R.,  
Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,  
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,  
Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and  
Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800

FEATURES  
source  
1. 650  
/organism="Litomosoides sigmodontis"  
/mol\_type="mRNA"  
/db\_xref="taxon:42156"  
/clone="JALSL3C109"  
/sex="mixed"  
/dev\_stage="infective L3"  
/clone\_lib="Litomosoides sigmodontis (parasitic nematode)  
infective L3"  
/note="Vector: Lambda Zap II; Site\_1: EcoRI (5'end);  
Site\_2: XhoI (3'end); Litomosoides sigmodontis is a  
filarial nematode parasite of rats. The library was  
constructed from vector-(Ornithonyssus bacoti) derived L3  
for Prof. David Taylor at the Centre for Tropical  
Veterinary Medicine, Edinburgh, UK"

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Uma Rao and David Bird  
(david\_bird@wustl.edu) at North Carolina State University. DNA  
Sequencing by: Washington University Genome Sequencing Center St.  
Louis.

Seq primer: T3 ET from Amersham  
High quality sequence stop: 269.

#### FEATURES

source  
Location/Qualifiers

1..327  
/organism="Meloidogyne incognita"  
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/dev\_stage="enriched for 2nd stage juveniles"  
/lab\_host="XLOI"  
/clone\_lib="Bird-Rao Meloidogyne incognita J2"  
/note="Vector: ZAP express - pBKCW (Stratagene); Site:1:  
EcoRI; Site:2: Oligo (dT) primed library. cDNA was  
constructed and cloned unidirectionally into the vector  
within the 5' EcoRI and 3' XhoI sites. This library was  
constructed by Dr. Uma Rao and Dr. David Bird at North  
Carolina State University."  
93 a 52 c 80 g 102 t

#### BASE COUNT

93 a 52 c 80 g 102 t

Query Match 17.5%; Score 301.4; DB 9; Length 327;  
Best Local Similarity 97.8%; Pred. No. 1.6e-62;  
Matches 316; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 503 CAACAAGTGGAGCTGTTTCTTGAACAACTTCTTCAATTTATGTTTCGGAAGATAGC 562  
Db 6 CCACAAGTGGAGCTGTTTCTTGAACAACTTCTTCAATTTATGTTTCGGAAGATAGC 64  
QY 563 GAGCAATGGCTACTATTACTGGACGTTATATGCAATGATAGGACAAAGATGGAGC 622  
Db 65 GAGCAATGGCTACTATTACTGGACGTTATATGCAATGATAGGACAAAGATGGAGC 124  
QY 623 GTATTAAGATGGCTTATGAGCAATTTGTTGGAGTATGACAAAAGCCACCGTTGATA 682  
Db 125 GTATTAAGATGGCTTATGAGCAATTTGTTGGAGTATGACAAAAGCCACCGTTGATA 184  
QY 683 AGGCTGCTGATGTTTACAGAGCGATATGCTCAATCTGAGACTGACGAATTTCTGAAC 742  
Db 185 AGGCTGCTGATGTTTACAGAGCGATATGCTCAATCTGAGACTGACGAATTTCTGAAC 244  
QY 743 CAATGCTGTTTTCGGACGATGGCGAGTAAAGATCAGCATCTCTTATTTCTTCAATT 802  
Db 245 CAATGCTGTTTTCGGACGATGGCGAGTAAAGATCAGCATCTCTTATTTCTTCAATT 304  
QY 803 ATGCTGCTGATGCTATGCTCAA 825  
Db 305 ATGCTGCTGATGCTATGCTCAA 327

#### RESULT 5

BJ112231 677 bp mRNA linear EST 23-JAN-2002  
LOCUS BJ112231 unpublished oligo-capped cDNA library, C. elegans L1 stage  
DEFINITION Caenorhabditis elegans cDNA clone yk1152e03 5', mRNA sequence.

#### ACCESSION

BJ112231.1 GI:18272281

#### VERSION

EST.

#### KEYWORDS

Caenorhabditis elegans

#### SOURCE

Caenorhabditis elegans

#### ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae

#### REFERENCE

1 (bases 1 to 677)  
Kohara, F., Shin, I., Thierri-Mieg, J., Thierri-Mieg, D., Suzuki, Y.  
and Sugano, S.  
A complementary view of the C. elegans genome  
Unpublished  
Contact: Tadashi Shin-i  
Center For Genetic Resource Information

National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

#### FEATURES

source

Location/Qualifiers

1..677  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk1152e03"  
/sex="hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="L1"  
/clone\_lib="unpublished oligo-capped cDNA library, C.  
elegans L1 stage"  
180 a 125 c 178 g 193 t 1 others

#### BASE COUNT

180 a 125 c 178 g 193 t 1 others

#### ORIGIN

Query Match 17.5%; Score 300.8; DB 12; Length 677;  
Best Local Similarity 67.7%; Pred. No. 3.1e-62;  
Matches 435; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

QY 17 TTGAGATGCAACAAATATCAAAATGTTCAACAAAAAGCTCTCTGTAGTTATGATGGAT 76  
Db 26 TGGCGATGCAAAATACAGTTCGGTGGCCAAATAGGTCTGTCTCATCTGTTATGATGGAT 85  
QY 77 GGGGCTTTCCGATGACACACAGCGAATGCAATGCTTAAGCTAAAGCTAAAGCCCTATTATGG 136  
Db 86 GGGGATTTCTGAAATCTTACGGTACGGTATTCTCAACGCACACAGACACAGTTATGG 145  
QY 137 ACAAACTTTGTTCTGAAATTCGCAAAATTCGAACACACAGCTCTCTCATGTTGGATTC 196  
Db 146 ACAGCTGTTCTGGGCAATTTGGCTCAAAATTTAGGCACATGCTCTCAATGTTGGTCTCC 205  
QY 197 CAGAGGCTTAATGGGAAATTTCTGAAGTTGGACATTTGAATATAGGAGCTGGAAGATTA 256  
Db 206 CAGAGGATTTGATGGGAAATTCGGAATTCGGAATTTGAACATCGGAGCGGACGTTTA 265  
QY 257 TTTATCAAGATTTGTTTCAATTAATTTGGCTGTTCAACGAACAGAGTTGTTCAAAATC 316  
Db 266 TCTATCAAGATTTGTTTCAATTAATTTGGCTGTTCAACGAACAGAGTTGTTCAAAATC 325  
QY 317 CTCAGATTTGCTCATCAGCTGAGCGTCAAGAGGAGTGTGTCATGTCATTTATTTAG 376  
Db 326 ACAGCTTGGTGGATGCTTCCGATCGCTTAAACGGAATGAGCTCTTCATCTGGCCG 385  
QY 377 GACTGTTAGCGATGGTGGTCCACTCTCATATATGATCATCTTTTGGTGGTATACGTG 436  
Db 386 GACTTGTCTGACGGAGGTGTTCTATTCATATTCATATTCATCATGTTGTTGTTTAAAG 445  
QY 437 CATTTAAACAATTACAGTGGCCAAAGGTTTTCATTCACCTTTTCTGCTGATGCTGAGATA 496  
Db 446 CCATCAAGAGCTCGGAGTTCAGAACTTTTCTTCTTACGAGAGTGTGCGTGA 505  
QY 497 CTTCCCAACAGCTGAGCTGCTTATCTTGAACAACTTCTTCAATTTATTTG ---CTTCGG 553  
Db 506 CTTCTCCAAACAGTGGAGTTGGATTCCTTGAACAACTTCTGAGTCTTGGAGAACTA 565  
QY 554 AAAAGTAGGAGAAATGGCTACTATCTAGTGGAGCTTATTTATGATGATAGGACAAA 613  
Db 566 CTGGATATGGAACACTAGCTACTGTAGTTGGCGCTACTATCTATGATGATCGGATAACA 625  
QY 614 GATGGAGCTATTAGATGGCTTATGAGCAATTTCTGGAGG 656  
Db 626 GATGGAGCTATTAGATGGCTTATGAGCAATTTCTGGAGG 668

#### RESULT 6

AU204921

LOCUS

DEFINITION

unpublished oligo-capped cDNA library, stage L4

655 bp mRNA linear

EST 17-JUL-2001

Caenorhabditis elegans cDNA clone yk843c10 5', mRNA sequence.

AU204921 GI:14836754  
EST.  
SOURCE  
ORGANISM  
*Caenorhabditis elegans*  
*Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea*  
; *Rhabditiidae; Peloderinae; Caenorhabditis*.  
1 (bases 1 to 655)  
Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
and Sugano,S.  
A complementary view of the C.elegans genome  
Unpublished  
Contact: Yuji Kohara  
Genome Biology Lab.  
National Institute of Genetics  
Yata 1111, Mishima, Shizuoka 411, Japan  
Tel: 81-559-81-6854  
Fax: 81-559-81-6855  
Email: yokohara@lab.nig.ac.jp.  
Location/Qualifiers  
1..655  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk843c10"  
/sex="Hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="L4"  
/clone\_lib="unpublished oligo-capped cDNA library, stage L4"

BASE COUNT 175 a 124 c 169 g 187 t

ORIGIN

Query Match 17.08; Score 292.6; DB 9; Length 655;  
Best Local Similarity 67.68; Pred. No. 3e-60;  
Matches 425; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

QY 17 TTGAGATGGACAATATCAAAATGTTCACAAAAGTCTGTTGTAGTTATTGATCGAT 76  
DB 27 TGGCGATGGCAATAACAGTTCGGTGCCCAATAGGTCTGTCTCATCGTTATGATGAT 86

QY 77 GGGGCCCTTCCGATGAACACACGGGAATGCAATTGCTAAAGCTAAACGCCTATTATGG 136  
DB 87 GGGGAGTTTCTGAAGATCCTTACGGTAACGCTATTCTCAACGCACACACCAGTTATGG 146

QY 137 ACAACTTGTCTTGGAAATGGCAAAATTTGGAAGCACACGGTCTTCATGTTGGATTC 196  
DB 147 ACAAGCTGTCTCGGGCAATTTGGGCTCAAATTTAGGCACATGGTCTTCATGTTGGTCTCC 206

QY 197 CAGAAGCTTAATGGGAATCTCGAGTTGGACATTTGAATATAGGAGCTTGGAGAGTTA 256  
DB 207 CAGAAGATTGATGGGAATTCGGAAGTCGGACATTTGAACATCGGACGGAGCTGTTA 266

QY 257 TTTATCAAGATATTGTTCGAATTAATTGCTGTTCACGAAGACGAGTTGTTACAAATC 316  
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QY 317 CTCAGATTGTCATCAGCTGAGCGTGCAAGAGGGAGTGTFCTGATTCGATTTATATAG 376  
DB 327 AGAGCTTGTGTGGATGCTTGGCGATCGTCTAAAAACGGAAATGGACGCTCTTCATCTGGCG 386

QY 377 GACTGGTTACCGATGGTGGTCCACHTCATATTGATCATCTTTTTCCGTTGATAGTG 436  
DB 387 GACTTGTCTGACGGAGGTGTCATTTCTCATATTGATCATGTTTTCGTTGGTTAAGG 446

QY 437 CATTTAAACAATTACAGTGCCAAAGGTTTTTCATTCACCTTTTTTCGTGATGGTGCAGTA 496  
DB 447 CCATCAAGAGCTCGGAGTTCAGAACTTTACCTTCATTTCTACGGAGATGGTCTGATA 506

QY 497 CTTCGCCAACAGTGGAGCTGGTTATCTTGAACAACCTCTTCATATTTATTG---CTTCGG 553

Db	507	CTTCTCCAAACAGTGGAGTTGGATTCTCTTGAACAAACCCCTCGAGTCTTCTTGGAGAAACTA	566
QY	554	AAAAGTACGAGAAATGGCTACTATTACTGACGCTTATTATGCAATGGATGAGGACAAA	613
Db	567	CTGATATGGAACACTAGCTACTGTAGTTGGCGCTACTATGCTATGATGCGGATAACA	626
QY	614	GATGGAGCGTATTAAAGATGGCTTATGAG	642
Db	627	GATGGAGCGCTATCAATGTGCTACGAG	655
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LOCUS	BJ121936		
DEFINITION	BJ121936 unpublished oligo-capped cDNA library, C. elegans L1 stage		
ACCESSION	BJ121936		
VERSION	BJ121936.1	GI:18282074	
KEYWORDS	EST.		
SOURCE	Caenorhabditis elegans		
ORGANISM	Caenorhabditis elegans		
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;		
AUTHORS	1 (bases 1 to 652)		
	Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.,		
	and Sugano, S.		
TITLE	A complementary view of the C.elegans genome		
JOURNAL	Unpublished		
COMMENT	Contact: Tadasu Shin-I Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.		
FEATURES			
source	Location/Qualifiers		
	1..652		
	/organism="Caenorhabditis elegans"		
	/mol_type="mRNA"		
	/strain="N2"		
	/db_xref="taxon:6239"		
	/clone="YK1282f07"		
	/sex="hermaphrodite"		
	/tissue_type="whole animal"		
	/dev_stage="L1"		
	/clone_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"		
BASE COUNT	173 a 124 c 168 g 187 t		
ORIGIN			
Query Match	16.9%	Score 290.6;	DB 12; Length 652;
Best Local Similarity	67.5%	Pred. No. 9.2e-60;	
Matches 423;	Conservative	0; Mismatches 201;	Indels 3; Gaps 1;
QY	17	TTGAGATGGACAATATCAAAATGTTTCAACAAAAGTCTCTTGTAGTTATTGATGGAT	76
Db	26	TGCGGATGGCAATAACACAGTTCGGTGSCCAATGAAGTCTCTCATCTGTTATGATGGAT	85
QY	77	GGGGCTTTCCGATGAACAACACGGGAATGCAATTCGTAAGCTAAACGCCCTATTATGG	136
Db	86	GGGGATTTTCTGAAGATCCCTAGGGTAACGCTATTCTCAACGCCACACACACAGTTATGG	145
QY	137	ACAACTTTGTTCTGGAAATTTGCCAAAATTTGGAACACACACGGTCTTCATGTTGGATTGC	196
Db	146	ACAAGCTGTGTTCGGGCAATTTGGGCTCAAAATGAGGCACATGGTCTTCATGTTGGTCTCC	205
QY	197	CAGAAGCCTTAATGGGAAATTCCTGAAGTTTGACATTTTGAATATAGGAGCTGGAAGAGTTA	256
Db	206	CAGAAGGATTGATGGGAAATTCGGAAGTCSGACATTTGAACATCGGAGCGGACGTGTTA	265
QY	257	TTTATCAAGATATGTTTGAATTAATTTGSGCTGTTCAACGAAACAGAGTTTGTGTACAAATC	316
Db	266	TCTATCAAGACATTTGCTGATTAATCTGGCAGTCAAGAACAACAAATTTGTGACTAATG	325

QY 317 CTCAGATGTTGTCATCAGCTGACGCTGCAAGAGGGAGCTGCTGATTCGATTTATTAG 376  
 DB 326 AGAGCTTGGTGGATGCTTGGATGCTGCTAAACCGAATGACGCTTCATCTGGCCG 385  
 QY 377 GACTGTTAGCGATGTTGGTGTCCACTCTCATATTGATCATCTTTTGGCTTGTATACGTG 436  
 DB 386 GACTTCTTCTGACGAGGTGTTCAATCTCATATTGATCATCATGTTTGGTTAAAG 445  
 QY 437 CATTAAACAATTAACAAGTCCCAAGGTTTTCATTCACATTTTTCGCTGTCGAGATA 496  
 DB 446 CCATCAAGAGCTCGGAGTTCAGAACTTTACCTTCATTCTACGAGATGTCGCGATA 505  
 QY 497 CTTCCGCAACAAGTGGAGTGTCTTCTTGAACAACCTTCTCAATTTATTG---CTTCGG 553  
 DB 506 CTTCTCCAAACAGCTGGAGTTGGATCTTGAACAACCCCTCGAGTTCTTGGAGAAACTA 565  
 QY 554 AAAAGTACGAGAAATGGCTTACTTACTGAGAGTATTATGCAATGGATAGGACAAA 613  
 DB 566 CTGGATATGGAACACTAGCTACTGTAGTTGGCGCTACTATGCTATGGATCGGATAACA 625  
 QY 614 GATGGAGCGCTATTAAAGTGGCTATG 640  
 DB 626 GATGGAGCGCTATCAATGTGCGATACG 652

## RESULT 8

BJ108160

LOCUS

DEFINITION BJ108160 649 bp mRNA linear EST 23-JAN-2002  
 Caenorhabditis elegans cDNA library, C. elegans L1 stage

ACCESSION

BJ108160

VERSION

1

KEYWORDS

EST

SOURCE

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae

1 (bases 1 to 649)

Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.

and Sugano, S.

A complementary view of the C.elegans genome

Unpublished

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. .649

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1104f08"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/clone\_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

BASE COUNT 174 a 124 c 165 g 186 t

ORIGIN

Query Match

Best Local Similarity 16.7%; Score 287.6; DB 12; Length 649;

Matches 421; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

QY 17 TTGAGATGACAAATATCAAAATGTTCAACAAAAGTCTGCTGTAGTTATTGATGGAT 76

DB 24 TGGCGATGCAATATACAGTTGGTGGCCCAATAGTCTGCTCATCTGTTATTGATGGAT 83

QY 77 GGGGCGCTTTCCGATGAACAACACGGAATGCTAAAGCTAAAGCCCTATTATGG 136  
 DB 84 GGGGAGTTTCTGAAGATCCTTACGGTACGCTATTCTCAACGCACAGACACCATGATGG 143  
 QY 137 ACAAACTTTGTTCTTGGAAATTTGGCAAAAATTTGGAACACACCGCTCTTCATGTTGGATTGC 196  
 DB 144 ACAAGCTGTGTTGGGCAATTTGGGCTCAAAATTTGAGGCACATGCTCTTCATGTTGGTCTCC 203  
 QY 197 CAGAAGCTTAATGGGAAATTTCTGAAGTTGGACATTTGAATATAGAGCTGGAGAGTTA 256  
 DB 204 CAGAAGATTTGATGGGAAATTTGGAAAGTCGGACATTTGAACATTCGAGCGGACGTTGTA 263  
 QY 257 TTTATCAAGATATTTGTCGAATTAATTTGGCTGTTTCAACGAAACGAGTTTGTATACAAATC 316  
 DB 264 TCTATCAACACATTTGTCGATTAATTTCTGCAGTCAAGAACAACAATTTGTGACATTAAG 323  
 QY 317 CTCAGATTTGTCATCAGCTGAGCGTGCAGAAAGAGGGAGTGGTGCATTTGATTTATTAG 376  
 DB 324 AGAGCTTGGTGGATGCTTGGGATCGTGTAAACGGAATGACGCTTCATCTGGCCG 383  
 QY 377 GACTGTTAGCGATGCTGCTCCACTCTCATATTGATCATCTTTTTCGTTGATACGTG 436  
 DB 384 GACTTGTCTTCTGACGGAGGTGTTTCATTCATATTGATCATGTTTGTGTTGTTAAGG 443  
 QY 437 CATTTAAACAATTAACAAGTCCCAAGGTTTTCATTCACATTTTTCGCTGATGGTCGAGATA 496  
 DB 444 CCATCAAGAGCTCGGAGTTCCAGAACTTTACCTACATTTCTACGGAGATGGTCGCGATA 503  
 QY 497 CTTGCGCAACAAGTGGAGCTGGTATCTTTGGAACAACCTTCTCAATTTATTG---CTTCGG 553  
 DB 504 CTTCTCCAACAGTGGAGTTGGATTCCTTTGAACAAACCCCTCGAGTTCTTGGAGAAACTA 563  
 QY 554 AAAAGTACGGAATTTGGCTACTATTACTGAGCTTATTATGCAATGGATAGGACAAA 613  
 DB 564 CTGGATATGAAAACCTAGCTACTGTTGGCGCTACTACTGATGATCGGATCGGATAACA 623  
 QY 614 GATGGAGCGCTATTAAAGATGGCTTA 638  
 DB 624 GATGGAGCGCTATCAATGTTGCGATA 648

## RESULT 9

CB374256

LOCUS

DEFINITION

ro99h09.y1.Heterodera glycines J3 Heterodera glycines cDNA 5',

similar to TR:O44742 O44742 F57B10.3 PROTEIN. [1] ; mRNA sequence.

CB374256

VERSION

CB374256.1

KEYWORDS

EST

SOURCE

Heterodera glycines

Heterodera glycines

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchida;

Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

1 (bases 1 to 647)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.

Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.

Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., R.

Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe

M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.

Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and

Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This library was generated by cloning cDNAs directionally into

Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and 7'/XhoI

are at the 3'-end). The library was excised [now in plasmid]

SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jpmcderm@iastate.edu).

Seq primer: T3 from Gibco  
High quality sequence stop: 469.

## FEATURES

source  
Location/Qualifiers

1..647

/organism="Heterodera glycines"

/mol\_type="mRNA"

/db\_xref="taxon:51029"

/sex="mixed"

/tissue\_type="whole organism"

/dev\_stage="3rd stage juvenile"

/lab\_host="DH10B"

/clone\_lib="Heterodera glycines J3"

/note=Vector: pBluescript SK+ (Stratagene); Site\_1: XhoI; Site\_2: EcoRI; This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI are at the 3'-end). The library was excised [now in pBluescript SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806).

Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jpmcderm@iastate.edu)."

168 a 151 c 171 g 157 t

## BASE COUNT

ORIGIN

Query Match 16.5%; Score 283; DB 14; Length 647;

Best Local Similarity 66.8%; Pred. No. 6.5e-58;

Matches 419; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Qy 491 GAGATCTGCCAACAGTGGAGCTGTTATCTTGACAACTCTTCAATTTATTGCTT 550

Db 1 GTGATACATGCCAACAGTGGAGCGGCTCTTGCACAACTCTTGACTTCTTAAGTG 60

Qy 551 CGGAAAGTAGCGGAGAAATGGCTACTATTAAGTACGACGTATATGCAATGATAGGAGCA 610

Db 61 CCGAAACTATGGCGAATTTGGCAACCATTTGTTGCTGTTATATGCCATGACCGTGACA 120

Qy 611 AAGATGGGCGGTAAAGATGCTTATGAGGCAATTTGGAGGTATTTGGACAAAAG 670

Db 121 ACCGATGGGCGGAATTAAGTGTCCACGAGGCAATTTGGTGGCGAGAGGGCGAAAGT 180

Qy 671 CCACCGTGTATAAGCTGTCTGATGTTGTAGACAGCATATGCTCAATCTGAGACTGACG 730

Db 181 CGCAACCGCGGAATGCTGTACAAATTTGTGACGAGCGCTAGCGCAACACAGACTGACG 240

Qy 731 AATTCTGAACCAATTTGTTTTTCGACGATGGCGAGTAAGAGATGACGATACTCTTA 790

Db 241 AATTCTGACGCCCATCGTGTGTTTCGACGAGCGCGTGTGAAGACAATGACACATGG 300

Qy 791 TTTTCTTCAATATCGCTGATGCTATGCTGCTCAAAATTTGTAATGTTGGG---TCTCG 847

Db 301 TCTTTTCAATATCGCTGATGCTGATGCTGATGCTGATTAACAAGTGGATGGTGTCTGC 360

Qy 848 AACCTTATAAGATTTAATAGTTTCGCTTCCTCACCTCAAAATATTACGATTTAGTGGGA 907

Db 361 AAAACCTGCAGGATTTGGCGACCAATGTGTGATTTCCGACGAGCTGCACATCAACGA 420

Qy 908 TGACCCCAATACAAAGAGTTTCCATTTCCATTCGTTATTCACCTGCTGACTCATCTA 967

Db 421 TGACACAGTACAAACGAGAGTTTCCATTTCCCATTCCTGTTCCCTCCGCTGACGCATAAA 480

Qy 968 ATGTGCTGTGTAATGCTGCTTCTCAAGGAGTTACTCAATTTTCACTGTGTCGGAACCTG 1027

Db 481 ATGTGCTGTGTAATGCTGCTTCTCAAGGAGTTACTCAATTTTCACTGTGTCGGAACCTG 540

Qy 1028 AGAAGATCTCTCATGTTTACCTTCTTCTTTAATGTTGTTGCGAAGAGTTCAATTTCCAAGAT 1087

Db 541 AAAAGATGTCCTATGCTGCTTCTTTTCAACGCTGGACGAGAGTGCATTTGAGGGTG 600

Qy 1088 AAGAGCGTTGTATGTTTCCGTCACCAA 1114

Db 601 AAGAACGCGAGTTCGTCCTCCATCGCGA 627

## RESULT 10

BO613449

LOCUS

DEFINITION

BO613449 285 bp mRNA linear EST 26-JUN-2002  
rd06h03.y1 Meloidogyne incognita egg SL1 TOPO v1 Meloidogyne  
incognita cDNA 5' similar to TR:044742 044742 F57B10.3 PROTEIN. [1]

;- mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Meloidogyne incognita (southern root-knot nematode)

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

1 (bases 1 to 285)

McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,

Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,

Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarelshvili,R.,

Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe

,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,

Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and

Wilson,R.

The Washington Univ. Nematode EST Project, 1999

Unpublished

CONTACT: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter

at Washington University, St. Louis. Meloidogyne incognita eggs

were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.

Putative full length read

The vector to vector length is 286

Seq primer: -40RP from Gibco.

Location/Qualifiers

1..285

/organism="Meloidogyne incognita"

/mol\_type="mRNA"

/db\_xref="taxon:6306"

/dev\_stage="egg"

/lab\_host="DH10B (Invitrogen)"

/clone\_lib="Meloidogyne incognita egg SL1 TOPO v1"

/note=Vector: pCRII-TOPO (Invitrogen); Site\_1: EcoRI;

Site\_2: EcoRI; The library was constructed by Claire

Murphy and Dr. James McCarter at Washington University,

St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR

products of size >400 nucleotides containing SL1 on the 5'

end and oligo(dT) on the 3' end were non-directionally

cloned into pCRII-TOPO(Invitrogen) following the TOPO TA

cloning protocol. Meloidogyne incognita eggs were provided

by Andrew Kloek of Divergence Inc., St. Louis, MO."

92 a 43 c 69 g 81 t

BASE COUNT

ORIGIN

Query Match 16.2%; Score 278.2; DB 13; Length 285;

Best Local Similarity 98.9%; Pred. No. 6.8e-57;

Matches 280; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 70 GATGATGGGCGCTTTCGATGAACACACACGGAATGCAATTCGTAAGCTAAACGCT 129

Db 2 GATGATGGGCGCTTTCGATGAACACACATGCAATTCGTAAGCTAAACGCT 61

Qy 130 ATTTGACAACTTTTGTCTGGAAATTTGGCAAAATTTGGAAGCACACGGTCTTCATGTT 189

Db 62 ATTTGACAACTTTTGTCTGGAAATTTGGCAAAATTTGGAAGCACACGGTCTTCATGTT 121

Qy 190 GGATTGCCAAGAGCTTAATGGGAAATTCCTGAAGTTGGACATTTTGAATATAGGAGCTGGA 249





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/db_xref="taxon:6239"
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/sex="hermaphrodite"
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elegans L1 stage"

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QY 883 CCTAAATATTCAGATTAGTGGGATGACCCCAATACAAATAAGAGATTCATTCATCG 942
Db 725 CCATCAATCTTCAAGTATATGGAATGACTACATACAAAGCCGAGTTCATCAATCG 666
QY 943 TTATTCACCTGTGACTCATATAATGTGCTGTGAATGGCTTCTTCTCAAGGATT 1002
Db 665 CTGTTCCCGCAGCATCGACAAATATGTTGGCTGAGTGGCTCCCGAGCAAAAGTT 606
QY 1003 ACTCAATTTCACTGCGGAACTGAGAAGTATCCATGTTACCTTCTTCTTAAATGGT 1062
Db 605 TCGCAATTTCACTGCGGAACTGAGAAGTATCCATGTTACCTTCTTCTTAAATGGT 546
QY 1063 GGTCTGAGAGTTCATTCAGATGAAGAGCGTTGTATGGTCCGTCACCAAAAGATT 1122
Db 545 GGACTTGAATGAATATTTGAGGAGAGAAAGTGTATGAGTCCCGAGTCCAA---AGGTN 489
QY 1123 GCTACATATGATTTAAACACAGAAATGAATGCTGCGGAGTTCGCGGAAATATGTCGAG 1182
Db 488 GCAACTTACGATCTTCAACAGAAATGCTGCGGCGGCTGCTGACAAATGATGAA 429
QY 1183 CAAATTTAGTCAGGAGGATCCTTTGGTTATGTGCAATTTTTCGCGCTCTGACATGGTT 1242
Db 428 CAACTCGAGGCTGGAATCATCATTCATTTATGTGCAACTTTTCTCCACCATATGGTC 369
QY 1243 GGACATATGTTAAATTTGAACCTGCGTCAAGCATGTCAAGTACTGACGAGCAAT 1302
Db 368 GGGCATCGGGAGTATGAGCTGTGCAAGGCTGTGNAAGTATGATATCGCAATC 309
QY 1303 GGAAGATATTTGAAGCATGCCAACTTATAATACGTTCTTATGGTTACTTCCGATCAT 1362
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REFERENCE
1 (bases 1 to 621)
AUTHORS
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE
A complementary view of the C.elegans genome
JOURNAL
Unpublished
COMMENT
Contact: Tadasu Shin-i
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Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
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Db 116 CTATTCTCAACGACAGACACAGCTATGGAAGCTGTGTCGGCAATGGGCTCAAA 175
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